

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 12, 2003, 14:59:17 ; Search time 97 Seconds  
(without alignments)  
1680.240 Million cell updates/sec

Title: US-09-804-472-2

Perfect score: 4177  
Sequence: 1 MDASSDPYLPYDGGGDNIPL.....DILRHMAQTANODPASIMFN 791.

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4037	96.6	818	4 014918	014918 homo sapien
2	4032	96.5	818	11 09R287	09R287 ratius norv
3	4002	95.8	760	6 018894	018894 oryctolagus
4	3993	95.6	791	13 09YH11	09YH11 xenopus lae
5	3984	95.4	760	11 P97274	P97274 cavia porce
6	3688.5	88.3	759	13 09PU16	09PU16 oreochromis
7	3148.5	75.4	746	6 09GKE7	09GKE7 sus scrofa
8	3145.5	75.3	746	6 09PTU3	09PTU3 oryctolagus
9	3109.5	74.4	746	11 099P66	099P66 cavia porce
10	3081	73.8	808	13 09PMK7	09PMK7 xenopus lae
11	3066	73.4	808	13 013080	013080 xenopus lae
12	3060.5	73.3	716	11 099J22	099J22 mus musculu
13	3031	72.6	840	13 09PU15	09PU15 oreochromis
14	2374.5	56.8	732	5 09YUY1	09YUY1 drosophila
15	2123	50.8	797	5 017804	017804 caenorhabdi
16	2116.5	50.7	796	5 09U6W4	09U6W4 caenorhabdi

17	1376	32.9	310	11 09WUG1	09WUG1 cavia porce
18	1020.5	24.4	772	5 060958	060958 leishmania
19	1015	24.3	812	3 060159	060159 schizosacch
20	771	18.5	796	5 09BHB2	09BHB2 caenorhabdi
21	748.5	17.9	758	4 09UJH7	09UJH7 homo sapien
22	735	17.6	812	4 096RY8	096RY8 homo sapien
23	728	17.4	772	10 081491	081491 arabisdopsis
24	728	17.4	792	10 P92943	P92943 arabisdopsis
25	714.5	17.1	811	5 09U6M6	09U6M6 caenorhabdi
26	709	17.0	667	3 094287	094287 schizosacch
27	697.5	16.7	869	6 09TT16	09TT16 oryctolagus
28	692	16.6	813	5 09V6D9	09V6D9 drosophila
29	684.5	16.4	764	10 P93567	P93567 solanum tub
30	681.5	16.3	1001	5 09BMK8	09BMK8 caenorhabdi
31	679	16.3	863	5 095VFR	095VFR dictyosteli
32	676	16.2	780	10 P92942	P92942 arabisdopsis
33	671.5	16.1	780	10 040485	040485 nicotiana t
34	670.5	16.1	775	10 064990	064990 arabisdopsis
35	669.5	16.0	775	10 093Y50	093Y50 arabisdopsis
36	668.5	16.0	775	10 P92941	P92941 arabisdopsis
37	667	16.0	779	10 096282	096282 arabisdopsis
38	663	15.9	745	5 095QNR	095QNR caenorhabdi
39	662	15.8	887	11 054822	054822 ratius norv
40	661	15.8	786	10 09XF71	09XF71 nicotiana t
41	652	15.6	907	11 054821	054821 ratius norv
42	646.5	15.5	1084	5 09BMK8	09BMK8 caenorhabdi
43	646	15.5	1046	5 095ZP4	095ZP4 caenorhabdi
44	646	15.5	1085	5 095ZP5	095ZP5 caenorhabdi
45	645.5	15.5	773	10 096325	096325 arabisdopsis

## ALIGNMENTS

## RESULT 1

ID 014918 PRELIMINARY: PRT: 818 AA.  
AC 014918;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Chloride channel protein 3.  
GN CLCN3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LENS EPITHELIUM;  
RA Rae J.L., Shepard A.R.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Huang P., Di A., Kaetzel M.A., Musch M.W., Xie W., Johnson X.D.,  
RA Nelson D.J.;  
RT "Molecular identification of human CLC-3 as the CAMKII-activated  
Chloride channel: A potential cystic fibrosis bypass pathway.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF029346; AAB95161.1; -  
DR EMBL; AF172729; AAD51034.1; -  
DR InterPro: IPR000644; CBS domain.  
DR InterPro: IPR001807; Cl-channel\_volt.  
DR Pfam: PF00571; CBS; 2.  
DR Pfam: PF00654; Voltage-CLC; 1.  
DR PRINTS; PR00762; CLCHANNEL.  
DR SMART; SM00116; CBS; 2.  
SQ SEQUENCE 818 AA; 90965 MW; 30FF0A6A2D6EF3B8 CRC64;

Query Match 96.6%; Score 4037; DB 4; Length 818;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 776; Conservative 1; Mismatches 10; Indels 12; Gaps 3;

QY	3	ASDDYVLEDDGG-----DNIPRLREHKGCTHYMTNGSINSSHHLLDDEPI	52
Db	22	ASSDEEL-LDGAAGVIMDFQTSEDONL-LDGGTAVGTHYMTNGSINSSHHLLDDEPI	79
QY	53	PGVGVYDDEPHITDWREKCKDRHRNRINSKKKESAMDMTKSLYDAMSGMLVYTLGLAS	112
Db	80	PGVGVYDDEPHITDWREKCKDRHRNRINSKKKESAMDMTKSLYDAMSGMLVYTLGLAS	139
QY	113	GALAGLLIDIAADNMHTDLKEGICLSALWYNHQQCCWGSNETTFFERDCKCPOMKIWAELITG	172
Db	140	GALAGLLIDIAADNMHTDLKEGICLSALWYNHQQCCWGSNETTFFERDCKCPOMKIWAELITG	199
QY	173	QAEGGGSYIMYIMYIMFALISFAFLAVSLVVFAPYACGSGIPEIKITLSGFIIRGLK	232
Db	200	QAEGGGSYIMYIMYIMFALISFAFLAVSLVVFAPYACGSGIPEIKITLSGFIIRGLK	259
QY	233	WTLMKTTTLVLAVASGLCKEGEDLVHVAACCGNIFSYLEPKYSTNEAKKREVLASASA	292
Db	260	WTLMKTTTLVLAVASGLCKEGEDLVHVAACCGNIFSYLEPKYSTNEAKKREVLASASA	319
QY	293	AGVSATFAPAPIGVYFSLSEVSYRPELTKMRSPFALVAFLVRSINPGRNSRILVFY	352
Db	320	AGVSATFAPAPIGVYFSLSEVSYRPELTKMRSPFALVAFLVRSINPGRNSRILVFY	379
QY	353	EYHPWVYFELFPELLGVEFGGLGCAFFIRANIAMCRRRKSTKGYLVLEVIITVAITA	412
Db	380	EYHPWVYFELFPELLGVEFGGLGCAFFIRANIAMCRRRKSTKGYLVLEVIITVAITA	439
QY	413	VIAPRNPYTRLNTSELKELTDCGPRESSSLCDYRDMNASKIVDIDPRPAGICVYSA	472
Db	440	VIAPRNPYTRLNTSELKELTDCGPRESSSLCDYRDMNASKIVDIDPRPAGICVYSA	499
QY	473	IWOCLALIFKIMTVPTFGIKVPSGFLFISMAIGATGRIVGIAVEQLAVYVHHDMFIK	532
Db	500	IWOCLALIFKIMTVPTFGIKVPSGFLFISMAIGATGRIVGIAVEQLAVYVHHDMFIK	559
QY	533	EMCEVGALCITPGLIYAWYGAACCGVYTRMTVSLVYVFEITGSELYVLAAYMTSKY	592
Db	560	EMCEVGALCITPGLIYAWYGAACCGVYTRMTVSLVYVFEITGSELYVLAAYMTSKY	619
QY	593	VGDAGRGIGIYEAHRLNGYFPEFLDAKEEFTHTYLAADVMPRRNDPLAVLTODNNMTVD	652
Db	620	VGDAGRGIGIYEAHRLNGYFPEFLDAKEEFTHTYLAADVMPRRNDPLAVLTODNNMTVD	679
QY	653	IENMINETSYNGFPVIMSKESQRLVGFALRDLTIAESARKKQEGIVGSSRVCFAQHP	712
Db	680	IENMINETSYNGFPVIMSKESQRLVGFALRDLTIAESARKKQEGIVGSSRVCFAQHP	739
QY	713	SLPASPPEPLKLSILMSPEPTVDHFMELIVDIEFKILROCIYTHNRRLLGITTKD	772
Db	740	SLPASPPEPLKLSILMSPEPTVDHFMELIVDIEFKILROCIYTHNRRLLGITTKD	799
QY	773	ILRHMAQTANODPASIMFN 791	
Db	800	ILRHMAQTANODPASIMFN 818	
RESULT 2			
QY	Q9R287	PREDIMINARY; PRT; 818 AA.	
AC	Q9R287;		
DT	01-MAY-2000 (Tremblrel. 13, Created)		
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)		
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)		
DE	Chloride channel protein 3 long form (Fragment).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY;		
XX	MEDLINE=20378002; PubMed=10915634;		

Query Match	Best Local Similarity	Matches 773: Conservative	Score 4032: DB 11: Length 818: Pred. No. 3,3e-318: Mismatches 10: Indels 12: Gaps 3:
3	ASSDPFLPYDGGG-----DNIPLELRKCTHYMTMGSSINSTHLLDDEPT	52	
22	ASDDEL-LDGAALMDPQTSDDNL-LDGDPAAGTHYMTMGSSINSTHLLDDEPT	79	
53	PGVGYTDFHTIDWYREKCKDREHRRIRNSKKESAMEKTKLYAASGMLVYTLGLAS	112	
80	PGVGYTDFHTIDWYREKCKDREHRRIRNSKKESAMEKTKSLYAWSGMLVYTLGLAS	139	
113	GALAGLIDIAAMMDLKGICLSALMYHBECCGNSNTTEEDRDKCQMTMELLIG	172	
140	GALAGLIDIAAMMDLKGICLSALMYHBECCGNSNTTEEDRDKCQMTMELLIG	199	
173	QAEQGSYIMNYIMYFMALSFALVASLVKVPAYACSGSIPETKITLSGITINGYLCK	232	
200	QAEQGSYIMNYIMYFMALSFALVASLVKVPAYACSGSIPETKITLSGITINGYLCK	259	
223	WTLMTKITLVLVAASGLSGKEGFLVHACCCGNFSTLPKYSMTNEAKKREVLASASA	292	
260	WTLMTKITLVLVAASGLSGKEGFLVHACCCGNFSTLPKYSMTNEAKKREVLASASA	319	
293	AGVSVAFGAPIGGVLEEVSYEPPLKTLMTSPFAALVAALVLRSLNPFGRSLVLEFYV	352	
320	AGVSVAFGAPIGGVLEEVSYEPPLKTLMTSPFAALVAALVLRSLNPFGRSLVLEFYV	379	
353	EYHTWYLFELFPFILLGVFGGLNCAFFIRAIAMCRRKSKTEGKPYLEVIYIAATA	412	
380	EYHTWYLFELFPFILLGVFGGLNCAFFIRAIAMCRRKSKTEGKPYLEVIYIAATA	439	
413	VIAPNPYRLMTSELIKELFTDGPRESSLCDYRNDNMASKIYDDIPDRAGIGVSA	472	
440	VIAPNPYRLMTSELIKELFTDGPRESSLCDYRNDNMASKIYDDIPDRAGIGVSA	499	
473	IWOCLALIEKTIIMTVFTFGIKVPSGLTIPSAIGALAGRIAGVLAEOALAYVHDMFIFK	532	
500	IWOCLALIEKTIIMTVFTFGIKVPSGLTIPSAIGALAGRIAGVLAEOALAYVHDMFIFK	559	
533	EMCEVGADCTTPGGLVAMGAACLGAVTRMTASLVVIYELGGLAEYIPLMAAAMTSKW	592	
560	EMCEVGADCTTPGGLVAMGAACLGAVTRMTASLVVIYELGGLAEYIPLMAAAMTSKW	619	
593	VGDAGREGIYEAHTRILNGVYPLDAKKEEFTHTTLADVWRPBRNDPPLAVLTLQDMNTYDD	652	
620	VGDAGREGIYEAHTRILNGVYPLDAKKEEFTHTTLADVWRPBRNDPPLAVLTLQDMNTYDD	679	
653	IENMINEYSYNCFPIYINKESORLVGFALRDLTIAISARKKOGCIYSSVYCAQHTP	712	
680	IENMINEYSYNCFPIYINKESORLVGFALRDLTIAISARKKOGCIYSSVYCAQHTP	739	
713	SLPAESPRLKRLSLDMSPTVDTHTPMEIYVDIFERRKLGLOCVLTNIGRLGITTKKD	772	
740	SLPAESPRLKRLSLDMSPTVDTHTPMEIYVDIFERRKLGLOCVLTNIGRLGITTKKD	799	
773	ILRHMAQTANODPASIMFN 791		
800	ILRHMAQTANODPASIMFN 818		

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RESULT 3
ID 018894 PRELIMINARY; PRT; 760 AA.
AC 018894:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chloride channel protein 3 (CLC-3).
GN CLCN3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=CORNEAL ENDOTHELIUM;
RA Rae J.L., Shepard A.R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL
CC CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY
CC TERM IN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-
CC -1- SIMILARITY: TO OTHER CHLORIDE CHANNELS.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC EMBL: AF029348; AAB95163.1; ALT_INIT.
CC InterPro: IPR000644; CBS_domain.
CC pfam: PF00571; CBS; 2.
CC pfam: PF00654; voltage_clc; 1.
CC PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 154 174 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
FT TRANSMEM 285 305 POTENTIAL.
FT TRANSMEM 330 350 POTENTIAL.
FT TRANSMEM 365 385 POTENTIAL.
FT TRANSMEM 442 462 POTENTIAL.
FT TRANSMEM 467 487 POTENTIAL.
FT TRANSMEM 508 528 POTENTIAL.
FT TRANSMEM 536 556 POTENTIAL.
FT DOMAIN 577 616 CBS 1.
FT DOMAIN 698 749 CBS 2.
SO SEQUENCE 760 AA; 84516 MW; 9B6DDA86296847E7 CRC64;

Query Match 95.8%; Score 4002; DB 6; Length 760;
Best Local Similarity 100.0%; Pred. No. 8.8e-316;
Matches 760; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 SGPEIKTIIISGFIIRGYLCKMTLMKTTILVLAVASGLSLGKEGPIVHVHACCCGNFSY 240
OY 272 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSLSEVSYPPDLKMLRSFFALV 331
DB 241 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSLSEVSYPPDLKMLRSFFALV 300
OY 332 AAFVLSINPFGNSRLVLEYEYHTPWYLFELPFIILGVFGILGMAFFIRANIAMCRR 391
DB 301 AAFVLSINPFGNSRLVLEYEYHTPWYLFELPFIILGVFGILGMAFFIRANIAMCRR 360
OY 392 KSTRFKGYPVLEYIVAVIAFAVAFPPYTRLNSELIKELFDCCGLESSSLCDYRNDM 451
DB 361 KSTRFKGYPVLEYIVAVIAFAVAFPPYTRLNSELIKELFDCCGLESSSLCDYRNDM 420
OY 452 NASKIVDDIPDRPAGIGVSAIMOLCLALFKIIMVFTFGIKVPSGLFISMAIGAIAG 511
DB 421 NASKIVDDIPDRPAGIGVSAIMOLCLALFKIIMVFTFGIKVPSGLFISMAIGAIAG 480
OY 512 RIVGIAEQLAYYHHDFIFKEWCEVGADCTIPGLYAMVGAACLGVTMTVSLVIVF 571
DB 481 RIVGIAEQLAYYHHDFIFKEWCEVGADCTIPGLYAMVGAACLGVTMTVSLVIVF 540
OY 572 ELTGLEIYIVPMAAVMTSKWGDAPRGEGIYEAHIRLNGYPLIDAKEETHTTLADVM 631
DB 541 ELTGLEIYIVPMAAVMTSKWGDAPRGEGIYEAHIRLNGYPLIDAKEETHTTLADVM 600
OY 632 RPRRNDPPLAVLQDNTVDIDEMINETSNGPVPINSKESORLVGFALRDLTIAES 691
DB 601 RPRRNDPPLAVLQDNTVDIDEMINETSNGPVPINSKESORLVGFALRDLTIAES 660
OY 692 ARKKQEGIVSSRVCEQAHTPSPSPAESPRPLKLSILDMSPFTVYDHTPMEIIVDFRKL 751
DB 661 ARKKQEGIVSSRVCEQAHTPSPSPAESPRPLKLSILDMSPFTVYDHTPMEIIVDFRKL 720
OY 752 GLRQCLVTHNGRLIGITTKRDLIRHMAQTANODPASTMFN 791
DB 721 GLRQCLVTHNGRLIGITTKRDLIRHMAQTANODPASTMFN 760

RESULT 4
OYH11 PRELIMINARY; PRT; 791 AA.
ID 09YH11;
AC 09YH11;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative chloride channel CLC-3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-DISTAL NEPHRON;
RA Lindenthal S.M.B.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y09941; CAAT1072.2; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR pfam: PF00571; CBS; 2.
DR pfam: PF00654; voltage_clc; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
SO SEQUENCE 791 AA; 88140 MW; 216B1B1ED2A8C4EA CRC64;

Query Match 95.6%; Score 3993; DB 13; Length 791;
Best Local Similarity 94.2%; Pred. No. 5e-315;
Matches 745; Conservative 26; Mismatches 20; Indels 0; Gaps 0;

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QY 61 FHTIDWREKCKDBRRHRINSKKKESAMEMTKSLYDASGMLVLTGLASGALAGLID 120
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FHTIDWREKCKDBRRHRINSKKKESAMEMTKSLYDASGMLVLTGLASGALAGLID 120
QY 121 IADWMTDLKRGICLSALWYHNEOCCWGSNETTEERDKCPQWKTWAEILITGOAEGPGSY 180
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 IADWMTDLKRGICLSALWYHNEOCCWGSNETTEERDKCPQWKTWAEILITGOAEGPGSY 180
QY 181 IMNIMYEMALSFAPLAVSLVKYFAPAPAGSGIPEIKITISGFIRYGLKMTLMITI 240
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 IMNIMYEMALSFAPLAVSLVKYFAPAPAGSGIPEIKITISGFIRYGLKMTLMITI 240
QY 241 TLVLAVASGLSGKEGRLVHVACCGNIFSYLFPKYSTNEAKKREVLASAAGSVAFG 300
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TLVLAVASGLSGKEGRLVHVACCGNIFSYLFPKYSTNEAKKREVLASAAGSVAFG 300
QY 301 APIGGVLSLEEVSYFPPLKTLKMSRFPALVAAYLKSINFGNSRLVLFVEYHTPYL 360
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 APIGGVLSLEEVSYFPPLKTLKMSRFPALVAAYLKSINFGNSRLVLFVEYHTPYL 360
QY 361 FELPELILGVEFGIMGAFIRANIAMCRKRSTFGKYPVLEVIYVAITVAIAFPNRY 420
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 FELPELILGVEFGIMGAFIRANIAMCRKRSTFGKYPVLEVIYVAIAITVAIAFPNRY 420
QY 421 TRLMTSELKELFTDCGPLESSSLCDYRNDMNASKIVDDIPDRAGIGVSAIMQCLAL 480
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 TRLMTSELKELFTDCGPLESSSLCDYRNDMNASKIVDDIPDRAGIGVSAIMQCLAL 480
QY 481 IEKIMVFTFGIVPGLSFLPISMAIGALAGRIYGLAEQOLAYHHDFITKEMCEVAD 540
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 IEKIMVFTFGIVPGLSFLPISMAIGALAGRIYGLAEQOLAYHHDFITKEMCEVAD 540
QY 541 CITPGLIYAMGAACLGVTMTVSLVYIVELTGLGLEYIPLMAAVMTSKWGDAGFRE 600
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 CITPGLIYAMGAACLGVTMTVSLVYIVELTGLGLEYIPLMAAVMTSKWGDAGFRE 600
QY 601 GIYFAHIRLNGYPLDLAKEEFTHTTLADVMPRRNDPPLAVLTQDMNTVDIENMINET 660
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 GIYFAHIRLNGYPLDLAKEEFTHTTLADVMPRRNDPPLAVLTQDMNTVDIENMINET 660
QY 661 SYNEPPIVMSKESQRIYGFALRDLTIAIESARKKOEIVSSRVCFAQHPSPSLPAESPR 720
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 SYNEPPIVMSKESQRIYGFALRDLTIAIESARKKOEIVSSRVCFAQHPSPSLPAESPR 720
QY 721 PLKRLSILMSPTVTDHTPMEIYVDIFRKLGLRQCLVTHNGRLGIIITKKDILRHMAQT 780
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 PLKRLSILMSPTVTDHTPMEIYVDIFRKLGLRQCLVTHNGRLGIIITKKDILRHMAQT 780
QY 781 ANODPASIMFN 791
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 781 ANODPASIMFN 791

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RESULT 5
P97274 PRELIMINARY; PRT; 760 AA.
ID P97274
AC P97274;
DT 01-NOV-1997 (TEMBLrel. 03, Created)
DT 01-MAY-1999 (TEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Volume-regulated outwardly-rectifying chloride channel.
GN CLC-3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hysticognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049352; PubMed=9389484;
RA Duan D., Winter C., Cowley S., Hume J R., Horowitz B.;
RT "Molecular identification of a volume-regulated chloride channel.";
RL Nature 390:417-421(1997).

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RN [2]
RP SEQUENCE FROM N.A.
RA Duan D., Winter C., Hume J.R., Horowitz B.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U83464; AAB88634.2;
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 760 AA; 84357 MW; DE8D017D1881A531 CRC64;
Query Match 95.4%; Score 3984; DB 11; Length 760;
Best Local Similarity 99.6%; Pred. No. 2,5e-314;
Matches 757; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 32 MTNGSINSSHTLDDLDEPIPGYGTDDFTIDWREKCKDBRRHRINSKKKESAMEM 91
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTNGSINSSHTLDDLDEPIPGYGTDDFTIDWREKCKDBRRHRINSKKKESAMEM 60
QY 92 TKSLYDAMSGMLVLTGLASGALAGLIDADWMTDLKRGICLSALWYHNEOCCWGSNE 151
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TKSLYDAMSGMLVLTGLASGALAGLIDADWMTDLKRGICLSALWYHNEOCCWGSNE 120
QY 152 TTEERDKCPQWKTWAEILITGOAEGPGSYIMNIMYEMALSFAPLAVSLVKYFAPYACG 211
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TTEERDKCPQWKTWAEILITGOAEGPGSYIMNIMYEMALSFAPLAVSLVKYFAPYACG 180
QY 212 SGIEPIKILSGFTIRGLKWTLMIKITTYLVAVASGLSGKRGPLVHVACCGNIFSY 271
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SGIEPIKILSGFTIRGLKWTLMIKITTYLVAVASGLSGKRGPLVHVACCGNIFSY 240
QY 272 LFPYSTNEAKKREVLASAAGSVAFGAPIGVLSLEEVSYFPPLKTLKMSRFPALV 331
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LFPYSTNEAKKREVLASAAGSVAFGAPIGVLSLEEVSYFPPLKTLKMSRFPALV 300
QY 332 AAFVLRISINPGNSRLVLFVEYHTPYLFPFILLGVEFGIMGAFIRANIAMCRR 391
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 AAFVLRISINPGNSRLVLFVEYHTPYLFPFILLGVEFGIMGAFIRANIAMCRR 360
QY 392 KSTFGKYPVLEVIYVAITVAIAFPNRYTRLNLSLKELFTDCGPLESSSLCDYRDM 451
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 KSTFGKYPVLEVIYVAITVAIAFPNRYTRLNLSLKELFTDCGPLESSSLCDYRDM 420
QY 452 NASKIVDDIPDRPAGIGVSAIMQCLALIRKIMTVFTGIRKPSGLFISMAIGAIAG 511
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 NASKIVDDIPDRPAGIGVSAIMQCLALIRKIMTVFTGIRKPSGLFISMAIGAIAG 480
QY 512 RIVGIAEQOLAYHHDFITKEMCEVGADCTTGLIYAMGAACLGVTMTVSLVYIVF 571
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 RIVGIAEQOLAYHHDFITKEMCEVGADCTTGLIYAMGAACLGVTMTVSLVYIVF 540
QY 572 ELTGLGLEYIPLMAAVMTSKWGDAGFREGLYEAHIRLNGYPLDLAKEEFTHTTLADVM 631
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 ELTGLGLEYIPLMAAVMTSKWGDAGFREGLYEAHIRLNGYPLDLAKEEFTHTTLADVM 600
QY 632 RPRNDPPLAVLTQDMNTVDIENMINETSYNGPPIVMSKESQRLVGFALRDLTIAIES 691
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 RPRNDPPLAVLTQDMNTVDIENMINETSYNGPPIVMSKESQRLVGFALRDLTIAIES 660
QY 692 ARKROEGIVSSRVCFAQHPSPSLPAESPRPLKLSIIDMSPTVTDHTPMEIYVDIFRKL 751
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 ARKROEGIVSSRVCFAQHPSPSLPAESPRPLKLSIIDMSPTVTDHTPMEIYVDIFRKL 720
QY 752 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 791
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 760

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RESULT 6
Q9PUI6 PRELIMINARY; PRT; 759 AA.
ID Q9PUI6

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AC Q9PUI6; 01-MAY-2000 (TRENBLREL. 13, Created)  
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Chloride channel CLC-3.  
 OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;  
 OC Cichlidae; Oreochromis.  
 NC NCBL\_TaxID=8127;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99185316; PubMed=10082675;  
 RA Miyazaki H., Uchida S., Takai Y., Hirano T., Marumo F., Sasaki S.;  
 RT "Molecular cloning of CLC chloride channels in Oreochromis mossambicus  
 and their functional complementation of yeast gene mutant.";  
 RL Biochem. Biophys. Res. Commun. 255:175-181(1999).  
 DR EMBL; AF182215; AAD56388.1; -;  
 DR InterPro; IPR000644; CBS.domain.  
 DR InterPro; IPR001807; Cl-channel\_volt.  
 DR Pfam; PF00571; CBS; 2.  
 DR Pfam; PF00554; voltage\_CLC; 1.  
 DR PRINTS; PR00762; CLCHANNEL.  
 DR SMART; SM00116; CBS; 2.  
 SQ SEQUENCE 759 AA; 84752 MW; 63A65CC13GBFD16 CRC64;

Query Match 88.3%; Score 3688.5; DB:13; Length 759;  
 Best Local Similarity 90.7%; Pred. No. 2.4e-290;  
 Matches 690; Conservative 40; Mismatches 28; Indels 3; Gaps 2;

QY 32 MTNGGSI-NSSTHLDLDEPIPGVGYDDPHIDWREKCKDERHRRINSKKSAME 90  
 1 MSGGAPSSSTHLDLDEPIPGVGYDDPHIDWREKCKDERHRRINSKKSAME 60  
 DB 61 FTNKLDAWSGMLVYTLGLASGALAGLIDADMMNDKEGCLSLTFNHEQCWTSN 120  
 QY 91 MKSLYDANSGLVYTLGLASGALAGLIDADMMNDKEGCLSLTFNHEQCWTSN 150  
 61 FTNKLDAWSGMLVYTLGLASGALAGLIDADMMNDKEGCLSLTFNHEQCWTSN 120  
 DB 151 EPTFEERDKCPQKTMWELIIGQEGSGVIMYIMYIFWALSFAFLVAVFAPYAC 210  
 121 EPTFEERDKCPQKTMWELIIGQEGSGVIMYIMYIFWALSFAFLVAVFAPYAC 180  
 DB 121 EPTFEERDKCPQKTMWELIIGQEGSGVIMYIMYIFWALSFAFLVAVFAPYAC 180  
 QY 211 GSGIPEIKITLISGIRGLGKWTLMKITTLLVAVASGLSKESPLVAVACCCNIFS 270  
 181 GSGIPEIKITLISGIRGLGKWTLMKITTLLVAVASGLSKESPLVAVACCCNIFS 240  
 DB 181 GSGIPEIKITLISGIRGLGKWTLMKITTLLVAVASGLSKESPLVAVACCCNIFS 240  
 QY 271 YLEPKYSTNEAKREVLSAASAGVAVFAPYIGVLSLEEVSYYPPLKTIIRSFPAAL 330  
 241 YLEPKYSTNEAKREVLSAASAGVAVFAPYIGVLSLEEVSYYPPLKTIIRSFPAAL 300  
 DB 241 YLEPKYSTNEAKREVLSAASAGVAVFAPYIGVLSLEEVSYYPPLKTIIRSFPAAL 300  
 QY 331 VAAVFRSLNPNFGNSRLVFEYEHFPMYLFELFPIILGVRGGLGAPFIRANIMCAR 390  
 301 VAAVFRSLNPNFGNSRLVFEYEHFPMYLFELFPIILGVRGGLGAPFIRANIMCAR 360  
 DB 301 VAAVFRSLNPNFGNSRLVFEYEHFPMYLFELFPIILGVRGGLGAPFIRANIMCAR 360  
 QY 391 RKSTGKPYVLEVIIVAAITAVIAPNPYTRNTSELKELFTDCCPLESSSLCYRND 450  
 361 RKSTGKPYVLEVIIVAAITAVIAPNPYTRNTSELKELFTDCCPLESSSLCYRND 420  
 DB 361 RKSTGKPYVLEVIIVAAITAVIAPNPYTRNTSELKELFTDCCPLESSSLCYRND 420  
 QY 451 MNAKSLVVDIPRPGAGTGYSAIMQCLALIRKIMTVTFPGIKVNSGLFISMAIGAIA 510  
 421 MNAKSLVVDIPRPGAGTGYSAIMQCLALIRKIMTVTFPGIKVNSGLFISMAIGAIA 478  
 DB 421 MNAKSLVVDIPRPGAGTGYSAIMQCLALIRKIMTVTFPGIKVNSGLFISMAIGAIA 478  
 QY 511 GRIVGAVPOLAYYHDFWTFKEMCEVGADCTPGIYAVVAAACGVTATMVSIVVIV 570  
 479 GRIVGAVPOLAYYHDFWTFKEMCEVGADCTPGIYAVVAAACGVTATMVSIVVIV 538  
 DB 479 GRIVGAVPOLAYYHDFWTFKEMCEVGADCTPGIYAVVAAACGVTATMVSIVVIV 538  
 QY 571 FELTGLEIVTPVLAAMVMTSKWVGAFGRBGIVEAHIRLNGYPFILDAKEEFTHTTLAADY 630  
 539 FELTGLEIVTPVLAAMVMTSKWVGAFGRBGIVEAHIRLNGYPFILDAKEEFTHTTLAADY 598  
 DB 539 FELTGLEIVTPVLAAMVMTSKWVGAFGRBGIVEAHIRLNGYPFILDAKEEFTHTTLAADY 598  
 QY 631 MRRRNDPPLAVLTQDNMTVDIENINETSNGFPVINSKESQRLVGRALRDLTIAIE 690  
 603 MRRRNDPPLAVLTQDNMTVDIENINETSNGFPVINSKESQRLVGRALRDLTIAIE 690

DB 599 MRRRNDPPLAVLTQDNMTVDIENINETSNGFPVINSKESQRLVGRALRDLTIAIE 658  
 QY 691 SARRKQEGIVGSSRVCEAQTPTSLPAESPRLKRLSLDMSPTVNDHPMETVIOIFK 750  
 DB 659 NARRKQEGIVGSSRVCEAQTPTSLPAESPRLKRLSLDMSPTVNDHPMETVIOIFK 718  
 QY 751 LGRQCLVTHNGRSLGITTKDILIRMAQOTANODPASIMFN 791  
 DB 719 LGRQCLVTHNGRSLGITTKDILIRMAQOTANODPASIMFN 759

RESULT 7  
 Q9GKE7 PRELIMINARY; PRT: 746 AA.

AC Q9GKE7; 01-MAR-2001 (TRENBLREL. 16, Created)  
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Outwardly rectifying chloride channel.  
 GN CLC-5.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 NC NCBL\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20545523; PubMed=10978325;  
 RA Dowland L.K., Luyckx V.A., Enck A.H., Leclercq B., Yu A.S.L.;  
 RT "Molecular Cloning and Characterization of an Intracellular Chloride  
 Channel in the Proximal Tubule Cell Line, LLC-PK1.";  
 RL J. Biol. Chem. 275:37765-37773(2000).  
 DR EMBL; AF274055; AAG29104.1; -;  
 DR InterPro; IPR000644; CBS.domain.  
 DR InterPro; IPR001807; Cl-channel\_volt.  
 DR Pfam; PF00571; CBS; 2.  
 DR Pfam; PF00554; voltage\_CLC; 1.  
 DR PRINTS; PR00762; CLCHANNEL.  
 DR SMART; SM00116; CBS; 2.  
 SQ SEQUENCE 746 AA; 83123 MW; 655E3ED45FC61229 CRC64;

Query Match 75.4%; Score 3148.5; DB:6; Length 746;  
 Best Local Similarity 76.8%; Pred. No. 1.5e-246;  
 Matches 574; Conservative 85; Mismatches 87; Indels 1; Gaps 1;

QY 45 LDLDLDEPIPGVGYDDPHIDWREKCKDERHRRINSKKSAMEMTSLYDANSGLV 104  
 1 MDLEPIPGVGYDDPHIDWREKCKDERHRRINSKKSAMEMTSLYDANSGLV 60.  
 DB 1 MDLEPIPGVGYDDPHIDWREKCKDERHRRINSKKSAMEMTSLYDANSGLV 60.  
 QY 105 VTLTGLASGALAGLIDADMMNDKEGCLSLTFNHEQCWTSNMTTFFEERDKCPQK 164  
 61 MTLTGLSSLAGLIDISAHMMNDKEGCLSLTFNHEQCWTSNMTTFFEERDKCPQK 120  
 DB 61 MTLTGLSSLAGLIDISAHMMNDKEGCLSLTFNHEQCWTSNMTTFFEERDKCPQK 120  
 QY 165 TMNELIIGQEGSGVIMYIMYIFWALSFAFLVAVFAPYACGSGIPEIKITLISG 224  
 121 TSNELIIGQEGSGVIMYIMYIFWALSFAFLVAVFAPYACGSGIPEIKITLISG 180  
 DB 121 TSNELIIGQEGSGVIMYIMYIFWALSFAFLVAVFAPYACGSGIPEIKITLISG 180  
 QY 225 IIRGYGKWTLMKITTLLVAVASGLSKESPLVAVACCCNIFSYPYLPKYSTNEAKR 284  
 181 IIRGYGKWTLMKITTLLVAVASGLSKESPLVAVACCCNIFSYPYLPKYSTNEAKR 240  
 DB 181 IIRGYGKWTLMKITTLLVAVASGLSKESPLVAVACCCNIFSYPYLPKYSTNEAKR 240  
 QY 285 EYLSAASAGVAVFAPYIGVLSLEEVSYYPPLKTIIRSFPAALVAVFVLSNPNFGN 344  
 241 EYLSAASAGVAVFAPYIGVLSLEEVSYYPPLKTIIRSFPAALVAVFVLSNPNFGN 300  
 DB 241 EYLSAASAGVAVFAPYIGVLSLEEVSYYPPLKTIIRSFPAALVAVFVLSNPNFGN 300  
 QY 345 SRLVFEYEHFPMYLFELFPIILGVRGGLGAPFIRANIMCARRKSTKREKYVLEY 404  
 301 SRLVFEYEHFPMYLFELFPIILGVRGGLGAPFIRANIMCARRKSTKREKYVLEY 360  
 DB 301 SRLVFEYEHFPMYLFELFPIILGVRGGLGAPFIRANIMCARRKSTKREKYVLEY 360  
 QY 405 IIVATVAVIAPNPYTRNTSELKELFTDCCPLESSSLCYRNDMNSKSLVDDIPDR 464  
 361 IIVATVAVIAPNPYTRNTSELKELFTDCCPLESSSLCYRNDMNSKSLVDDIPDR 419  
 DB 361 IIVATVAVIAPNPYTRNTSELKELFTDCCPLESSSLCYRNDMNSKSLVDDIPDR 419  
 QY 465 AGIGVSAIMQCLALIRKIMTVTFPGIKVNSGLFISMAIGAIAIGRIVGAVPOLAYY 524

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Db 420 AGAGVYSAMQALATLLIKIYITFTFGMKIPSGLFIPSMVGAIAAGLLVGHMEQLAY 479
QY 525 HHDFIREKMEVGCADCTTGPLYAMVGAACLGVTMTVSLVYIVFELTGLGYIYPLM 584
Db 480 HHDMTIFNSWCSQACDCTTGPLYAMVGAACLGVTMTVSLVYIVFELTGLGYIYPLM 539
QY 585 AAVMTSKWGDAGFREGIEYEAHRLNGYPLFLDAKEEFTHTTLADVMRPRNDPLAVLT 644
Db 540 AAAMTSKVVADALRGEGYDAHRLNGYPLFLDAKEEFAHKTLAMDVKPRNDPLAVLT 599
QY 645 QDNMTVDDIEMNINETSNGFPVYMSKESQRLVGFALRDLTIAESARKKQEGIVGSSR 704
Db 600 QDSMTVEDVETIISETTYSGFPVYVRSQRLVGFALRDLTIIENARKKQDGVSTSI 659
QY 705 VCFQOHPSLPASPRPKLSIILDMSPFTDHTPMEIVVDIFRKGLRCLVTHNGRL 764
Db 660 IYFTHSPMPYPPTPKLKNLIDLSPTVDTLPMETIVDIFRKGLRCLVTHNGRL 719
QY 765 LGITTKKDLRHMATANODPASIMFN 791
Db 720 LGITTKKDVLRKHAQMANODPDSILFN 746

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## RESULT 8

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Q9TTU3 ID Q9TTU3 PRELIMINARY: PRT: 746 AA.
AC Q9TTU3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chloride channel CLC-5.
GN CLCN5.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM ZEALAND WHITE; TISSUE=CORNEA EPITHELIA;
RA Rae J.L.;
RT "Ion Channels in Cornea Epithelia.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF195523; AAF06018.1;
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl_channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83206 MW; 667F2701C0BF006A CRC64;

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Query Match 75.3%; Score 3145.5; DB 6; Length 746;

Best Local Similarity 77.0%; Pred. No. 2.5e-246; Mismatches 87; Indels 1; Gaps 1;

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QY 45 LDLDDEPIPGVGYDDPFTIDMWREKCKDRERHRIRNSKKKESAMETKSLYDAMSGLV 104
Db 1 MDLFEPIPGVGYDDPFTIDMWREKCKDRERHRIRNSKKKESAMETKSLYDAMSGLV 60
QY 105 VTLTGLASGALAGLIDIAADMTDLKRGICLSALVYHNECCWGSNETTEERDKCPQWK 164
Db 61 MLTLGLFSGSLAGLIDISAHMTDLKRGICGCFMFNFHEHCNMSNVTEFEDTKCEPN 120
QY 165 TWAALLIGAGGPGSSYIMNYIMYIFMALSPFAFLVSLVKVAPYACGSGIPEITILISGF 224
Db 121 SMSOLLNTEGAFAYIVNFYVLMALFAFLAVSLVKVAPYACGSGIPEITILISGF 180
QY 225 IIRGYLKMWTLMITITLVLAVASGLSLGKGPLVHVAACCGNIFSYLFPYSTNEAKR 284
Db 181 IIRGYLKMWTLMITITLVLAVASGLSLGKGPLVHVAACCGNILCHRFNKYRKNNEAKR 240
QY 285 EVLSAASAGVSAFAGPAGIGVLFSEEVSYFPLKTLMSFFAALVAAPVLRISINFGN 344

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Db 241 EYLSAAAAGVSAFAGPAGIGVLFSEEVSYFPLKTLMSFFAALVAAPVLRISINFGN 300
QY 345 SRLVLFVEYETPMYLPFLPFIILLGVGCLMGAFPIRANIAMCKRRKSTFGGYPILEV 404
Db 301 SRLVLFVEYETPMYLPFLPFIILLGVGCLMGAFPIRANIAMCKRRKSTFGGYPILEV 360
QY 405 IIVAITAVIAFPNYPYRLNTSELIKELFTDCGPLESSSLCDYRNDNASKIVDDIDPR 464
Db 361 LIVAITAIALAFPMYRMTSELISLNFDCGLDSSKLDENRFTSKGA-DLDRP 419
QY 465 AGIGVSAIMQCLALLFKITIMYFTGIRKYPGSLFIPSAIGAIAGIYCIANVQLAY 524
Db 420 AGVGYNAMQALALIKIYITFTFGMKIPSGLFIPSMVGAIAAGLLVGHMEQLAY 479
QY 525 HHDFIREKMEVGCADCTTGPLYAMVGAACLGVTMTVSLVYIVFELTGLGYIYPLM 584
Db 480 HHDMTIFNSWCSQACDCTTGPLYAMVGAACLGVTMTVSLVYIVFELTGLGYIYPLM 539
QY 585 AAVMTSKWGDAGFREGIEYEAHRLNGYPLFLDAKEEFTHTTLADVMRPRNDPLAVLT 644
Db 540 AAAMTSKVVADALRGEGYDAHRLNGYPLFLDAKEEFAHKTLAMDVKPRNDPLAVLT 599
QY 645 QDNMTVDDIEMNINETSNGFPVYMSKESQRLVGFALRDLTIAESARKKQEGIVGSSR 704
Db 600 QDSMTVEDVETIISETTYSGFPVYVRSQRLVGFALRDLTIIENARKKQDGVSTSI 659
QY 705 VCFQOHPSLPASPRPKLSIILDMSPFTDHTPMEIVVDIFRKGLRCLVTHNGRL 764
Db 660 IYFTHSPMPYPPTPKLKNLIDLSPTVDTLPMETIVDIFRKGLRCLVTHNGRL 719
QY 765 LGITTKKDLRHMATANODPASIMFN 791
Db 720 LGITTKKDVLRKHAQMANODPDSILFN 746

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## RESULT 9

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Q99P66 ID Q99P66 PRELIMINARY: PRT: 746 AA.
AC Q99P66;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chloride channel CLCN5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Cornejo I., Cid L.P., Sepulveda F.V.;
RT "Cloning and intestinal expression of guinea pig CLC-5 chloride
channel.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF326968; AAG49590.1;
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl_channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83093 MW; 92FC8AFDC7D8DA45 CRC64;

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Query Match 74.4%; Score 3109.5; DB 11; Length 746;

Best Local Similarity 76.2%; Pred. No. 2.1e-243; Mismatches 89; Indels 1; Gaps 1;

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QY 45 LDLDDEPIPGVGYDDPFTIDMWREKCKDRERHRIRNSKKKESAMETKSLYDAMSGLV 104
Db 1 MDLFEPIPGVGYDDPFTIDMWREKCKDRERHRIRNSKKKESAMETKSLYDAMSGLV 60
QY 105 VTLTGLASGALAGLIDIAADMTDLKRGICLSALVYHNECCWGSNETTEERDKCPQWK 164
Db 105 VTLTGLASGALAGLIDIAADMTDLKRGICLSALVYHNECCWGSNETTEERDKCPQWK 164

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Db 61 MILLIGLSSGLAGLIDISAHMMTDLKEGICTEGFMEFNEHCCWNSQOVTEDRDKCPEN 120
QY 165 TWAELLIGAEPSGYIMNYIMYIFALSFAFLAVSLVVPAPYAGSGSIPETKTLSSG 224
Db 121 SMSQLINNDGAPAYIVYEMVLMALLFAFLAVSLVVPAPYAGSGSIPETKTLSSG 180
QY 225 IIRGYLKWTLMTKTTTTLAVASGLSLGKESGPLVHVACCCGNIFSYLEPKYSTNEAKR 284
Db 181 IIRGYLKWTLMTKTTTTLAVASGLSLGKESGPLVHVACCCGNILCHCNKRYRENAKR 240
QY 285 EYLSAASAGSVAVGAPRGVLSLEEVSYYEPLKTLRSEFPALVAFVLRSLNPFEN 344
Db 241 EYLSAASAGSVAVGAPRGVLSLEEVSYYEPLKTLRSEFPALVAFVLRSLNPFEN 300
QY 345 SRLVYFVEYHPTMYLLEFPILLGVGGLGAFIRANIMCRKRKSTKGYKPYLEV 404
Db 301 SRLVYFVEYHPTMYLLEFPILLGVGGLGAFIRANIMCRKRKSTKGYKPYLEV 360
QY 405 IIVAAITAVIAFPNPYRLNLSLKEFLTDCGPLLESSLCDYRNDMAKSTIVDDIPDR 464
Db 361 IIVAAITAVIAFPNPYRLNLSLKEFLTDCGPLLESSLCDYRNDMAKSTIVDDIPDR 419
QY 465 AGIGYSAIMOLCLALIFKILMTFTFGIKVPSGLFIPSMATGATAGTIVGAVOGLAY 524
Db 420 AGIGYSAIMOLCLALIFKILMTFTFGIKVPSGLFIPSMATGATAGTIVGAVOGLAY 479
QY 525 HHDMFIFKEMCEVGAACITPGLYAMVGAACLGVTGMTVSLVIVFELTGLLEYVPLM 584
Db 480 HHDMFIFKEMCEVGAACITPGLYAMVGAACLGVTGMTVSLVIVFELTGLLEYVPLM 539
QY 585 AAVMTSKWVGDAFGREGIYEAHIRLNGYFELDAKEEFTHTTLAADVMPRRNDPPLAVLT 644
Db 540 AAVMTSKWVGDAFGREGIYEAHIRLNGYFELDAKEEFTHTTLAADVMPRRNDPPLAVLT 599
QY 645 ODNMTVDDIENNINFTSVNGSPVIMSKESORLVGFALRDLTATESARKKQEGVSSR 704
Db 600 ODNMTVDDIENNINFTSVNGSPVIMSKESORLVGFALRDLTATESARKKQEGVSSR 659
QY 705 VCFACHTPSLPAESPRLKLSILMSPPTVVDHTPMEIVDIFKRLGLRQCLVTHNGRL 764
Db 660 VCFACHTPSLPAESPRLKLSILMSPPTVVDHTPMEIVDIFKRLGLRQCLVTHNGRL 719
QY 765 LGITTKKDLRMAOTANODPASIMFN 791
Db 720 LGITTKKDLRMAOTANODPASIMFN 746

RESULT 10
Q9PMK7 PRELIMINARY: PRT: 808 AA.
AC 09PMK7.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chloride channel ClC-5.
GN ClC-5.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RC Mo L., Hellmich H.L., Fong P., Wood T.G., Embesi J., Willis N.K.;
RT "Comparison of amphibian and human ClC-5: Similarity of functional
RT properties and inhibition by external pH.";
RL J. Membr. Biol. 186:0-0(1999).
DR EMBL: AF063904; AAD24497.1; -
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR InterPro: IPR001130; TatD_DNase.
DR Pfam: PF00571; CBS; 2.

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DR Pfam: PF00654; voltage_Clc; 1.
DR PRINTS: PR00762; ClCHANNEL.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS01137; TatD; 1; UNKNOWN; 1.
SQ SEQUENCE 808 AA; 90068 MW; C3F1ADC759BD1676 CRC64;

Query Match 73.8%; Score 3081; DB 13; Length 808;
Best Local Similarity 71.5%; Pred. No. 4,8e-241;
Matches 563; Conservative 105; Mismatches 99; Indels 20; Gaps 3;

QY 22 ELHKRGTHNTM-----NGGSINSTHLLDLDEPIFGVGYDFFHTI 64
Db 25 ETTEATLDFMTDDVDPIDRDMAAGFVSNGNLGAKVMDFLD--VGVGYEDFNTI 82
QY 65 DWVRECKRREHRRRNSKKESAMETSKLYDAMSGMLVLTGLASALAGLIDIAAD 124
Db 83 DWVREKSRDRDNRHRELSKSTALHSDAFSGMMLLIGLTASLGLIDISSH 142
QY 125 WMTDLKEGICLSALWYNHQCCGWSNETTFFERDKCPQKWTMAELLIGAEPSGYIMNY 184
Db 143 WMTDLKEGICLPWFMEFNEHCCQWSNNVTFEDRNNCPERSMSQVLGRSEGAFFILMY 202
QY 185 IYVITFALSFAFLAVSLVVPAPYAGSGSIPETKTLSSGFIIRGYLKWTLMTKTTTTLV 244
Db 203 IYVITFALSFAFLAVSLVVPAPYAGSGSIPETKTLSSGFIIRGYLKWTLMTKTTTTLV 262
QY 245 AVASGLSLGKESGPLVHVACCCGNIFSYLEPKYSTNEAKKREYLSAASAGSVAVGAPRG 304
Db 263 AVSSGLSLGKESGPLVHVACCCGNILCHLTFRKNKREYLSAASAGSVAVGAPRG 322
QY 305 GVLFSLEEVSYYEPLKTLRSEFPALVAFVLRSLNPFENSRVLYEYVHPWYLFELF 364
Db 323 GVLFSLEEVSYYEPLKTLRSEFPALVAFVLRSLNPFENSRVLYEYVHPWYLFELF 382
QY 365 PELLIGREGLGAGFIRANIMCRKRKSTKGYKPYLEVIIYAATVIAFPNPYRLN 424
Db 383 PELLIGREGLGAGFIRANIMCRKRKSTKGYKPYLEVIIYAATVIAFPNPYRLN 442
QY 425 TSELKELFTDCGPLLESSLCDYRNDMAKSTIVDDIPDRPAGIGYSAIMOLCLALIFK 484
Db 443 SSEMSELFPDGLDSSKLCIDYVNDYNTK--GGLPDRPAANGYTTAMQSLALIFKA 501
QY 485 IMTVFTFGIKVPSGLFIPSMATGATAGTIVGAVOGLAYHHDMFIFKEMCEVGAACITP 544
Db 502 VITFTFGIKVPSGLFIPSMATGATAGTIVGAVOGLAYHHDMFIFKEMCEVGAACITP 561
QY 545 GLYAMVGAACLGATGMTVSLVIMFELTGLLEYIVPLMAAMTSKWVADALGRGSIVD 604
Db 562 GLYAMVGAACLGATGMTVSLVIMFELTGLLEYIVPLMAAMTSKWVADALGRGSIVD 621
QY 605 AHIRLNGYFELDAKEEFTHTTLAADVMPRRNDPPLAVLTODNMTVDDIENNINFTSYNG 664
Db 622 AHIRLNGYFELDAKEEFTHTTLAADVMPRRNDPPLAVLTODNMTVDDIENNINFTSYNG 681
QY 665 FPIVVSRESQRLMGFLVRDLTATESARKKQEGIVSTRIVFTHTPTPTAPPSLKL 724
Db 682 FPIVVSRESQRLMGFLVRDLTATESARKKQEGIVSTRIVFTHTPTPTAPPSLKL 741
QY 725 RSTLMSPTVVDHTPMEIVDIFKRLGLRQCLVTHNGRLGLITRKDLRMAOTANOD 784
Db 742 RAIMDLSPTTVDHTPMEIVDIFKRLGLRQCLVTHNGRLGLITRKDLRMAOTANOD 801
QY 785 PASIMFN 791
Db 802 PDSILEN 808

RESULT 11
O13080 PRELIMINARY: PRT: 808 AA.
AC O13080.
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

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DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
DE Chloride channel ClC-5.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-DISTAL NEPHRON;  
RA Lindenthal S.M.B., Schneider S., Ehrenfeld J., Willis N.K.;  
RT Cloning and functional expression of a ClC Cl-channel from renal cell  
RT line A6.  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y09940; CA71071.1; -  
DR InterPro: IPR000644; CBS\_domain.  
DR InterPro: IPR001807; Cl-channel\_volt.  
DR InterPro: IPR001130; Tald\_DNase.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF00654; voltage\_CLC; 1.  
DR PRINTS; PR00762; CLCHANNEL.  
DR SMART; SM00116; CBS; 2.  
DR PROSITE; PS01137; TATD; 1; UNKNOWN\_1.  
SQ SEQUENCE 808 AA; 89998 MW; C7AC12A3615D9712 CRC64;

Query Match 73.4%; Score 3066; DB 13; Length 808;  
Best Local Similarity 71.0%; Pred. No. 8e-240;  
Matches 559; Conservative 108; Mismatches 100; Indels 20; Gaps 3;

QY 22 ELAKRGHTMT-----NGSINSTHLDDLDEIPVGYDDPHTI 64  
DB 25 ETEATLDFMTDVPDRIDMAGFVSYNGAKYMDPLD--VPVGYEDPHNTI 82  
QY 65 DWRECKDEERRRRIRSKKESAMENTKSLYDAMSGMLVLTGLASGLAGLIDIAAD 124  
DB 83 DWREKSRDRDRREILSRKSESTMALHVSAPFSCHMLMLIGLTAGSLAGLIDISSH 142  
QY 125 WMTDLKGLCLSLAMYNHCOCCGNSNETTFEERDKCPQWKTMAELIIGAEGPGSYIMNY 184  
DB 143 WMTDLKGLCLPWFMEFHCOCCGNSNVTTFEDRNCPEWMSQOLVGRSEGAFFYTLNY 202  
QY 185 IMYIFMALSPAFILAVSLVKFAPYACGSGIPETKTLISGLTIGYCKWMLMTITVL 244  
DB 203 FMVVMALFSLAVLILVNFAPYACGSGIPETKTLISGLTIGYCKWMLMTITVL 262  
QY 245 AVASGSLGKEGFLVHVACCCGNIFFSLPKYSTNEAKKEVELSAASAGVSAFGAPIG 304  
DB 263 AVASGSLGKEGFLVHVACCCGNIFFSLPKYSTNEAKKEVELSAASAGVSAFGAPIG 322  
QY 305 GVLFSLSEVSYRPLKTLMSFPAALVAALVLRSLNFGNSRLVLEVEYHTFWYLELF 364  
DB 323 GVLFSLSEVSYRPLKTLMSFPAALVAALVLRSLNFGNSRLVLEVEYHTFWYLELF 382  
QY 365 PELLVFGGIMGAFPLRAIIMCRRKSKPKGYRPLEYIYAATTAVALFNPYTRLN 424  
DB 383 PELLVFGGIMGAFPLRAIIMCRRKSKPKGYRPLEYIYAATTAVALFNPYTRLN 442  
QY 425 TSELIELKELFDGPLESSSLCDYRNDMNSKIYDDIPDRPAGIGVSAIMQCLALIFKI 484  
DB 443 SSMSIELKELFDGPLESSSLCDYRNDMNSKIYDDIPDRPAGIGVSAIMQCLALIFKI 501  
QY 485 IMVFFPGIKVPSGLFIPSAIGAIGRIYVIGVLEQIAYYHDMFTFKEMCEVAGDCITP 544  
DB 502 VITLFFPGIKVPSGLFIPSAIGAIGRIYVIGVLEQIAYYHDMFTFKEMCEVAGDCITP 561  
QY 545 GLVAMGAACGAGVTMTSLVIVIFELTGLGLEYIVPLMAAMTSKWVADAGREGIVE 604  
DB 562 GLVAMGAACGAGVTMTSLVIVIFELTGLGLEYIVPLMAAMTSKWVADAGREGIVE 621  
QY 605 AHTRLNGYPLDAKEPTHTTTLADYVRRPRNPPLAVLIDQNMFTYDDIENMINTSYNG 664  
DB 622 AHTRLNGYPLDAKEPTHTTTLADYVRRPRNPPLAVLIDQNMFTYDDIENMINTSYNG 681

QY 665 PVIAMKESQRLVGFALRDLTIAIESARKKQEGIVSGSSVYCAQHTPSPAPSPRLKL 724  
DB 682 PVIYVSESQRLVGFALRDLTIAIESARKKQEGIVSGSSVYCAQHTPSPAPSPRLKL 741  
QY 725 RSLIDMSPEFTVDTHTPEIYVDIFRKLGLROCLVTHNGRLGLITTKDILRHMAQTNOD 784  
DB 742 RALIDMSPEFTVDTHTPEIYVDIFRKLGLROCLVTHNGRLGLITTKDILRHMAQTNOD 801  
QY 785 PASIMFN 791  
DB 802 PDSILFN 808

## RESULT 12

Q99J22 PRELIMINARY; PRT; 716 AA.

ID 099J22;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
DE Putative chloride channel (similar to Mm Clcn4-2).  
GN CLCN4-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC005553; AA05553.1; -  
DR MGI; MGI:104571; Clcn4-2.  
DR InterPro: IPR000644; CBS\_domain.  
DR InterPro: IPR001807; Cl-channel\_volt.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF00654; voltage\_CLC; 1.  
DR PRINTS; PR00762; CLCHANNEL.  
DR SMART; SM00116; CBS; 2.  
SQ SEQUENCE 716 AA; 80155 MW; C77B3EB48E3D7092 CRC64;

Query Match 73.3%; Score 3060.5; DB 11; Length 716;  
Best Local Similarity 74.7%; Pred. No. 1.9e-239;  
Matches 558; Conservative 82; Mismatches 76; Indels 31; Gaps 1;

QY 45 LDLDLDEIPGVGYDDPHNTIDWVRECKDERRRIRSKKESAMENTKSLYDAMSGMLV 104  
DB 1 MDLLEEFPPVGYEDPHNTIDWVRECKDERRRIRSKKESAMENTKSLYDAMSGMLV 60  
QY 105 VLTGLASGLAGLIDIAADWMTDLKGLCLSLAMYNHCOCCGNSNETTFEERDKCPQW 164  
DB 61 MLTIGLAGTLAGVIDLAVDMMTDLKGLCLSLAMYNHCOCCGNSNETTFEERDKCPQW 120  
QY 165 TMAELIIGAEGPGSYIMNYIMYIFMALSPAFILAVSLVKFAPYACGSGIPETKTLISG 224  
DB 121 KMSLELDSOEGASATILMTITLWMLFAPLAVSLVRFAPYACGSGIPETKTLISG 180  
QY 225 IIRGYLKWMTLTKITTLVLAASGLSLGKEGFLVHVACCCGNIFFSLPKYSTNEAKR 284  
DB 181 IIRGYLKWMTLTKITTLVLAASGLSLGKEGFLVHVACCCGNIFFSLPKYSTNEAKR 240  
QY 285 EYLSAASAGVSAFGAPIGGVFLSEVSYRPLKTLMSFPAALVAALVLRSLNFGN 344  
DB 241 EYLSAASAGVSAFGAPIGGVFLSEVSYRPLKTLMSFPAALVAALVLRSLNFGN 300  
QY 345 SRLVLFVEYHTFWYLELFPELLGVFGGLMGAFFIRANIAMCRRKSKPKGYRPLEY 404  
DB 301 SRLVLFVEYHTFWYLELFPELLGVFGGLMGAFFIRANIAMCRRKSKPKGYRPLEY 329  
QY 405 IIVAAITVAIFPNPYTRLNLSLIELKELFDGPLESSSLCDYRNDMNSKIYDDIPDR 464  
DB 330 IIVAAITVAIFPNPYTRLNLSLIELKELFDGPLESSSLCDYRNDMNSKIYDDIPDR 389  
QY 465 AGIGVSAIMQCLALIFKIIMVFFPGIKVPSGLFIPSAIGAIGRIYVIGVLEQIAYY 524



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Db 390 AGVGYTTAMQDIALALIRKIVTITFTFMKIKIPSGIFIPSMAGAMAGRWGIGVQDLAYH 449
Oy 525 HHDFIFKEMCEVAGADCTITPGLYAWGAACGLGVTBMTVSLVIVFELTGLSEVITPLM 584
Db 450 HHDMIIIFRWKCPGADCTITPGLYAWGAACGLGVTBMTVSLVIVFELTGLSEVITPLM 509
Oy 565 AAVMTSKWVGAFREGIYEAHIRLNGYPELDAKEEHTHTTLAADMVBRNDPPLAVLT 644
Db 510 AAAYTSKVVADAFKEGIEYEAHILNGYPELVDKDEFTHRLATVDMVRPREPLSLVLT 569
Oy 645 QDMNVVDDIENKINTSYNGPPVIMSKSQRLLVGLRDLTALIESARKKOEIGVSSR 704
Db 570 QDSMTVEVEVETLIKETDNGEPVLVRSERLIGFQRRELLAKMARQREGIVSNSI 629
Oy 705 VCFAGHTSLPAESPRLKSLIDMSPEVTVDHTPMEIVDIFPKLGRCLVTHNGRL 764
Db 630 MYTFEPEPELANSHPHLKRLINLSPTVYDHTPMTVYDIFKRLGRCLVTHNGRL 689
Oy 765 LGITTKDILRMACTANODPASIMFN 791
Db 690 LGITTKDILRMACTANODPASIMFN 716

RESULT 13
O9PUI5 PRELIMINARY; PRT; 840 AA.
AC O9PUI5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chloride channel CLC-5.
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
OC Clariidae; Oreochromis.
CC NCBI_TaxID=8127;
RN (1)
RP MEDLINE=99185316; PubMed=10082675;
RA Miyazaki H., Uchida S., Takai Y., Hirano T., Marumo F., Sasaki S.;
RT "Molecular cloning of CLC chloride channels in Oreochromis mossambicus
RT and their functional complementation of yeast CLC gene mutant.";
RL Biochem. Biophys. Res. Commun. 255:175-181(1999).
DR EMBL; AF182216; AAD56389.1; -.
DR InterPro; IPR000644; CBS domain.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 840 AA; 92293 MW; 81B9996E446F9605 CRC64;

Query Match 72.6%; Score 3031; DB 13; Length 840;
Best Local Similarity 71.8%; Pred. No. 5.8e-237;
Matches 562; Conservative 103; Mismatches 108; Indels 10; Gaps 4;

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Oy 251 SLGKEGPIVHVACCCGNIFSYLFPEKYSTNEAKRREVLSAASAGVAFGAPIGVLSL 310
Db 298 SLGKGPPLVHVACCCGNIFSYLFPEKYSTNEAKRREVLSAASAGVAFGAPIGVLSL 357
Oy 311 BEVSYFPLKTLMSRFPAALVAAPVLRISINPGNSRLVEVEYHTPWYLFELPFTILG 370
Db 358 BEVSYFPLKTLMSRFPAALVAAPVLRISINPGNSRLVEVEYHTPWYLFELPFTILG 417
Oy 371 VEGGLMGAFITRANTANCKRRKSTFGKYPLVEYITVAITAVIAFPNPTRLNLSLKL 430
Db 418 IFGLMGALFIAKANTAMCKRLKRTTCLGHVPEYEVVAALTAALLSYPMSTYMSGSELIS 477
Oy 431 ELFTDCGPLESSLDYNDNMASK--IVDDIPDPAGIGVSAIMOLCLALIFKIMTY 488
Db 478 ELFNCSLLDSQGLCYQNPATSDQVGNLSADRPAGLCTALMALALVEFKMITY 537
Oy 489 FTGKITVPSGLFIPSMAGIAGRIVGTAVEOLAYVHHDFIFKEMCEVAGADCTITPGLYA 548
Db 538 ITFGMKVPSGLFIPSMAGIAGRIVGTAVEOLAYVHHDFIFKEMCEVAGADCTITPGLYA 597
Oy 549 MYGAACAGVTRMTVSLVIVFELTGLSEYIVPLMAAVMTSKWVGAFREGIYEAHIR 608
Db 598 MYGAACAGVTRMTVSLVIVFELTGLSEYIVPLMAAVMTSKWVGAFREGIYEAHIR 657
Oy 609 LNYGPEPLDAKEEHTHTTLAADMVBRNDPPLAVLTODNMVDDIENMI NETSYNGFVI 668
Db 658 LNYGPEPLDAKEEHTHTTLAADMVBRNDPPLAVLTODNMVDDIENMI NETSYNGFVI 717
Oy 669 MSKESQRLVGFALRDLTALIESARKKOEIGVSSRCPAHTPSLPALSPRLKSLTL 728
Db 718 VSSERQRLVGFALRDLTALIESARKKOEIGVSSRCPAHTPSLPALSPRLKSLTL 777
Oy 729 DMSPTVVDHTPMEIVDIFPKLGRCLVTHNGSLLGITTKDILRMACTANODPASIM 788
Db 778 DMSPTVVDHTPMEIVDIFPKLGRCLVTHNGSLLGITTKDILRMACTANODPASIM 837
Oy 789 MFN 791
Db 838 LFN 840

RESULT 14
O9VUY1 PRELIMINARY; PRT; 732 AA.
AC O9VUY1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG5284 protein.
GN CG5284.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CC NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe C.R., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Bokoyva D., Botchan M.R., Bouck J., Broksstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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QY 115 LAGLIDADWMTDLKESICLSALWYNHOCWGSNETTFEERDKCPOMKTWAEIJGOA 174  
115 LAGLIDADWMTDLKESICLSALWYNHOCWGSNETTFEERDKCPOMKTWAEIJGOA 174  
Db 128 TAGIIDIGARMMSDIKTVGCADRFWDHHCMSNDTFYKD-DDCKAATKPMML--NY 184  
128 TAGIIDIGARMMSDIKTVGCADRFWDHHCMSNDTFYKD-DDCKAATKPMML--NY 184  
QY 175 EGPBSYI---NMWIMYIFWALSFAFLAVSLVKVFAVPYACGSGIPEIKTILSGFIIRGYLG 231  
175 EGPBSYI---NMWIMYIFWALSFAFLAVSLVKVFAVPYACGSGIPEIKTILSGFIIRGYLG 231  
Db 185 YNSSFLEFLEWIMYIFWALSFAFLAVSLVKVFAVPYACGSGIPEIKTILSGFIIRGYLG 244  
185 YNSSFLEFLEWIMYIFWALSFAFLAVSLVKVFAVPYACGSGIPEIKTILSGFIIRGYLG 244  
QY 232 KWTLMIKTITTLVLAASGLSGESGLVHVAOCNIFSYLFPKYSTNKAKEVLSAAS 291  
232 KWTLMIKTITTLVLAASGLSGESGLVHVAOCNIFSYLFPKYSTNKAKEVLSAAS 291  
Db 245 KMTFLIKSVGLISASGLSGESGLVHVAOCNIFSYLFPKYSTNKAKEVLSAAS 304  
245 KMTFLIKSVGLISASGLSGESGLVHVAOCNIFSYLFPKYSTNKAKEVLSAAS 304  
QY 292 AAGVAVAGAPIGVLFLEESYVFPPLKTLMSRFFALVAFAVRSINPFGNSRLVLFY 351  
292 AAGVAVAGAPIGVLFLEESYVFPPLKTLMSRFFALVAFAVRSINPFGNSRLVLFY 351  
Db 305 AAGVAVAGAPIGVLFLEESYVFPPLKTLMSRFFALVAFAVRSINPFGNSRLVLFY 364  
305 AAGVAVAGAPIGVLFLEESYVFPPLKTLMSRFFALVAFAVRSINPFGNSRLVLFY 364  
QY 352 VEYHTPWTFLEFPLILLGVGGLWGAFFIRANIAMCRKRSTK-FGKYPVLEVIIVAAI 410  
352 VEYHTPWTFLEFPLILLGVGGLWGAFFIRANIAMCRKRSTK-FGKYPVLEVIIVAAI 410  
Db 365 VDYMKKMTFIEIVPFAIIGLFGIIGSLFIFANIRMSFRKSKMLGPNPIYEVMLITLV 424  
365 VDYMKKMTFIEIVPFAIIGLFGIIGSLFIFANIRMSFRKSKMLGPNPIYEVMLITLV 424  
QY 411 TAVIAFPNRYRLNSELKELFTDC-GPLESSLCDYRNDMNAKIVDDIPDRAGIGV 469  
411 TAVIAFPNRYRLNSELKELFTDC-GPLESSLCDYRNDMNAKIVDDIPDRAGIGV 469  
Db 425 TAAISYFNPFTKSAQSMIOQLFDRCDQIDEDSLCDQNKALST----- 468  
425 TAAISYFNPFTKSAQSMIOQLFDRCDQIDEDSLCDQNKALST----- 468  
QY 470 YSAIWOLCLALFKIIMTVFTGIVKPSGLFIPSMAGIAGRIVIAVEOL-----AY 523  
470 YSAIWOLCLALFKIIMTVFTGIVKPSGLFIPSMAGIAGRIVIAVEOL-----AY 523  
Db 469 --AFQOLMALIFKVIITIFFGIIVPCGLFVPSICMGAIAGRIIGITVDQIFRAVOATP 526  
469 --AFQOLMALIFKVIITIFFGIIVPCGLFVPSICMGAIAGRIIGITVDQIFRAVOATP 526  
QY 524 YHHDMFIREMCEVAGADCTPGIYAMVGAACLGAVTRMTVSLVIVFELTGGLEYIVPL 583  
524 YHHDMFIREMCEVAGADCTPGIYAMVGAACLGAVTRMTVSLVIVFELTGGLEYIVPL 583  
Db 527 GHSDYFT---CQIGKDCVMFGIYAMVGAACLGAVTRMTVSLVIVFELTGGLEYIVPT 582  
527 GHSDYFT---CQIGKDCVMFGIYAMVGAACLGAVTRMTVSLVIVFELTGGLEYIVPT 582  
QY 584 MAAVMTSKWGDAGFREGIYEAHTRNGYPRLDAKEEFTHTLADVMRP----- 633  
584 MAAVMTSKWGDAGFREGIYEAHTRNGYPRLDAKEEFTHTLADVMRP----- 633  
Db 583 MVAIMFSKMWIGISKMGIEYEAHTRNGYPRLDASKEYPYSTVASOVMPRSIHROVADEM 642  
583 MVAIMFSKMWIGISKMGIEYEAHTRNGYPRLDASKEYPYSTVASOVMPRSIHROVADEM 642  
QY 634 -----RRNDPPLAVLTQDNMTVDIENMI NETSYNGFVIMSKESQRLVGFALRDLTIA 688  
634 -----RRNDPPLAVLTQDNMTVDIENMI NETSYNGFVIMSKESQRLVGFALRDLTIA 688  
Db 643 SMSDLRELKNEISVTEGSMILGDESLRQTDENGFPVVSQNSMHLVGFITRRDILLA 702  
643 SMSDLRELKNEISVTEGSMILGDESLRQTDENGFPVVSQNSMHLVGFITRRDILLA 702  
QY 689 IESAKKKEGIVGSSRVCFQOHTPSLPAESPPRLKRSILDSPTVTVDHPTMETIVDIF 748  
689 IESAKKKEGIVGSSRVCFQOHTPSLPAESPPRLKRSILDSPTVTVDHPTMETIVDIF 748  
Db 703 LHTAKKTOPYVYVTSIAVFSQVDPAMPGAPRLRLKILDMAPMTVTDQTPMETVIDMF 762  
703 LHTAKKTOPYVYVTSIAVFSQVDPAMPGAPRLRLKILDMAPMTVTDQTPMETVIDMF 762  
QY 749 RKLGLROCLVTHNGRLGIITRKDILRHMAQTANO 783  
749 RKLGLROCLVTHNGRLGIITRKDILRHMAQTANO 783  
Db 763 RKLGLRHVLTNGKVLGIIITKKDILQPMRNKNSQ 797  
763 RKLGLRHVLTNGKVLGIIITKKDILQPMRNKNSQ 797

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